

University of Groningen

## Genome-based phylogenetic analysis of *Streptomyces* and its relatives

Alam, Mohammad Tauqueer; Merlo, Maria Elena; Takano, Eriko; Breitling, Rainer

*Published in:*  
Molecular Phylogenetics and Evolution

*DOI:*  
[10.1016/j.ympev.2009.11.019](https://doi.org/10.1016/j.ympev.2009.11.019)

**IMPORTANT NOTE:** You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

*Document Version*  
Publisher's PDF, also known as Version of record

*Publication date:*  
2010

[Link to publication in University of Groningen/UMCG research database](#)

### *Citation for published version (APA):*

Alam, M. T., Merlo, M. E., Takano, E., & Breitling, R. (2010). Genome-based phylogenetic analysis of *Streptomyces* and its relatives. *Molecular Phylogenetics and Evolution*, 54(3), 763-772.  
<https://doi.org/10.1016/j.ympev.2009.11.019>

### **Copyright**

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

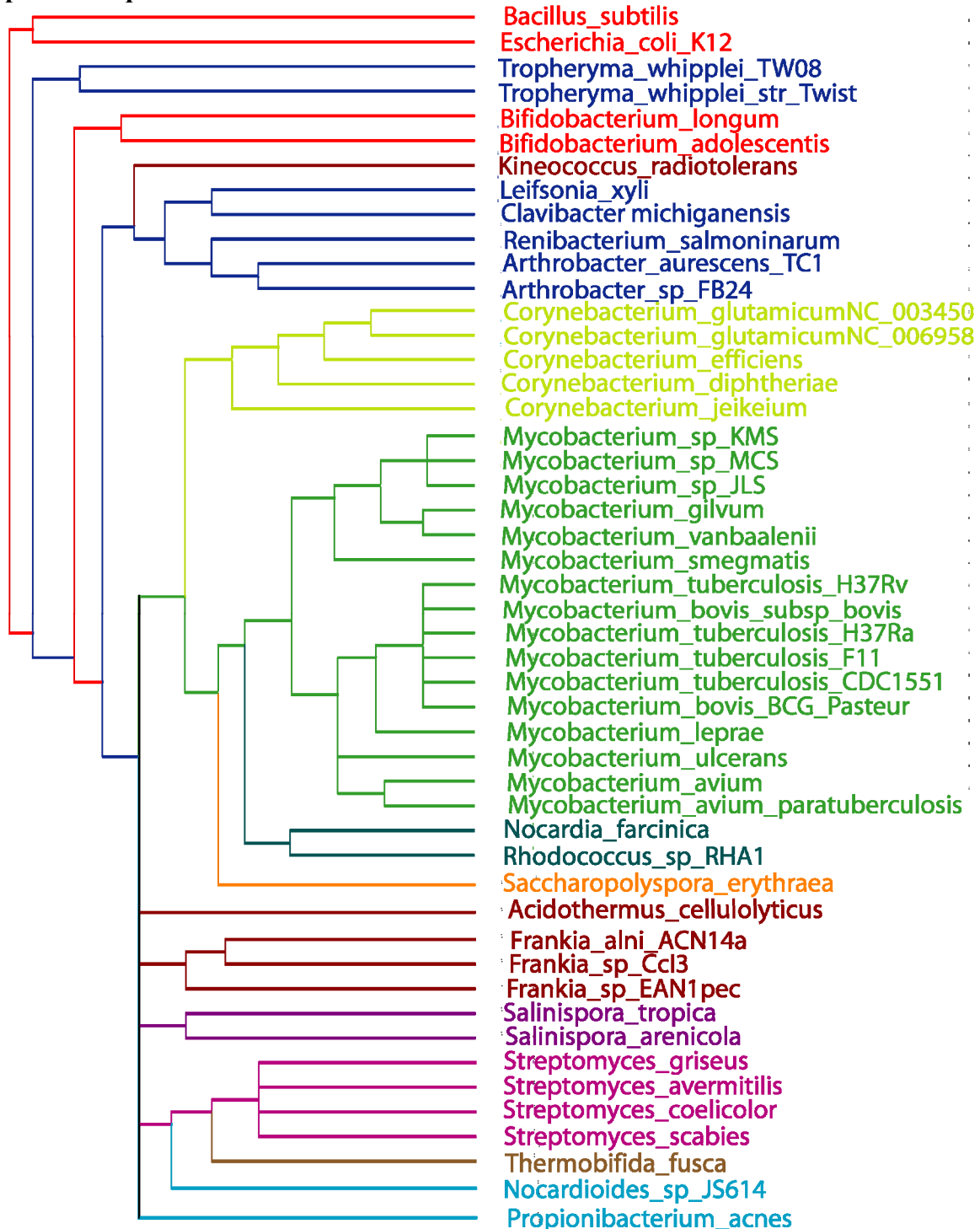
The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

### **Take-down policy**

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

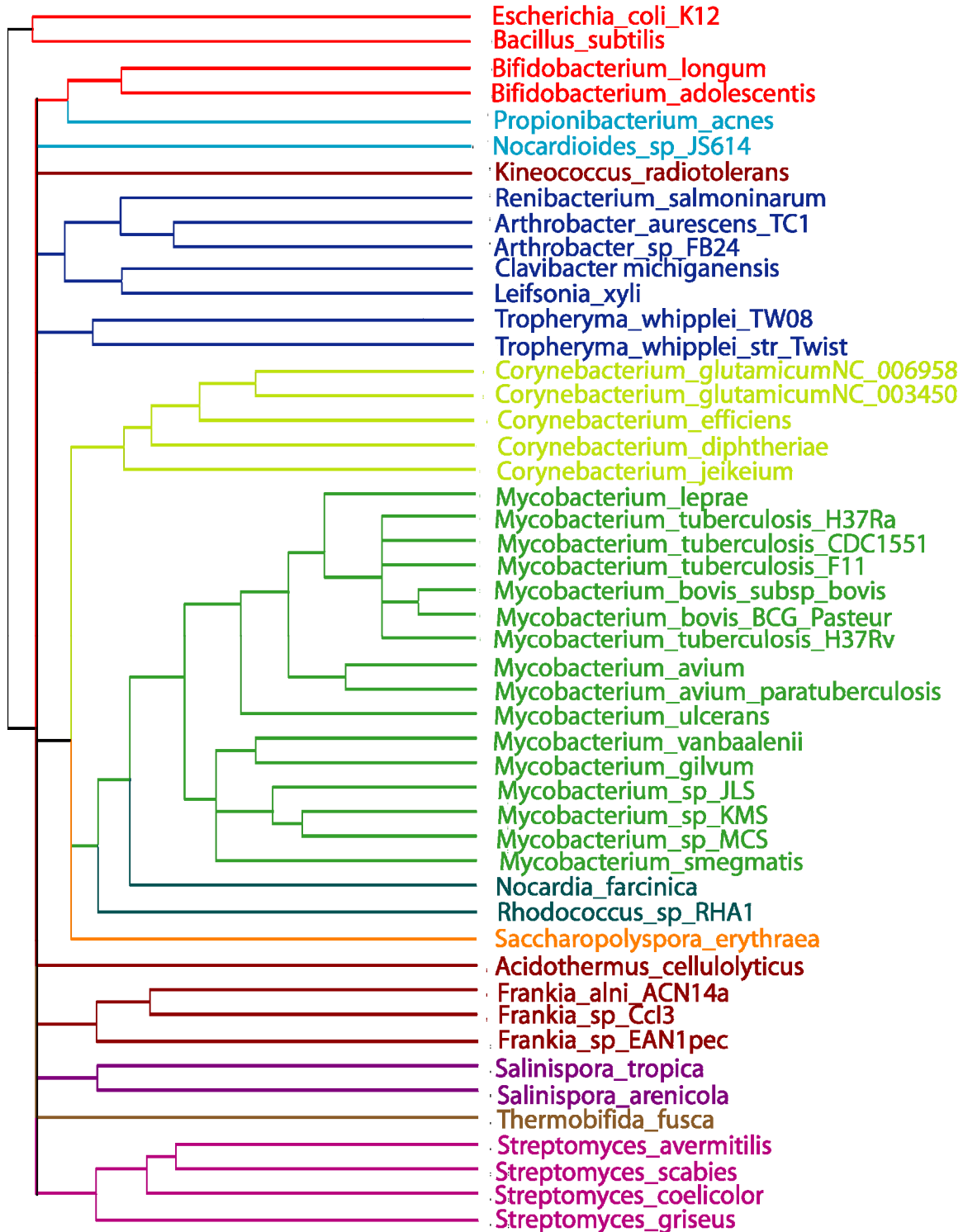
*Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.*

**Supplementary Material Fig 1. Consensus tree based on DNA Topoisomerase protein sequence**



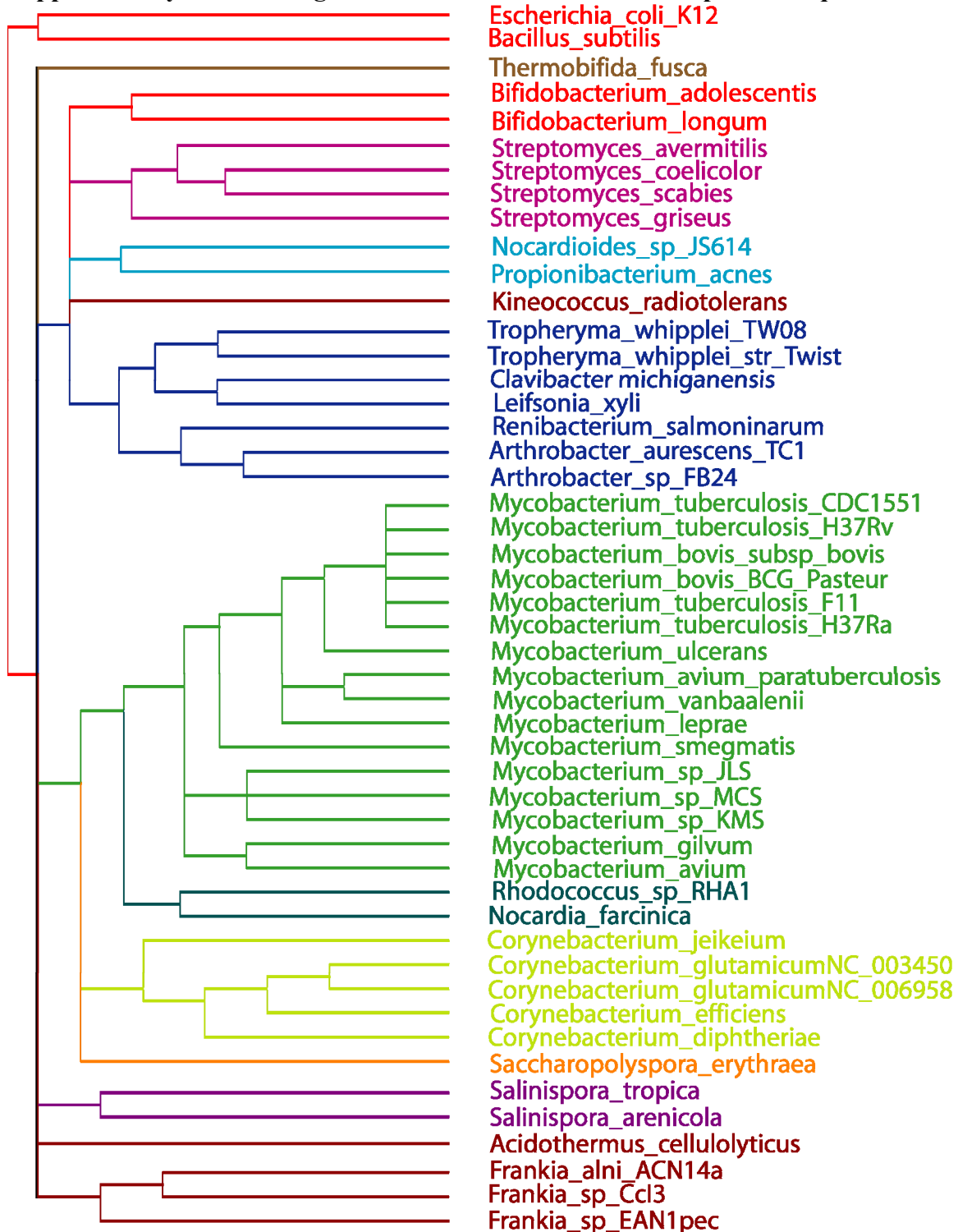
Initial trees were reconstructed using four tree inference approaches (NJ, Fitch, ML, PARS) with 100 bootstrap replicates each and combined by majority-rule consensus to include only well-supported branches. Organisms having the same colors are members of the same suborder in the taxonomical classification of NCBI.

**Supplementary Material Fig 2. Consensus tree based on GTPase protein sequence**



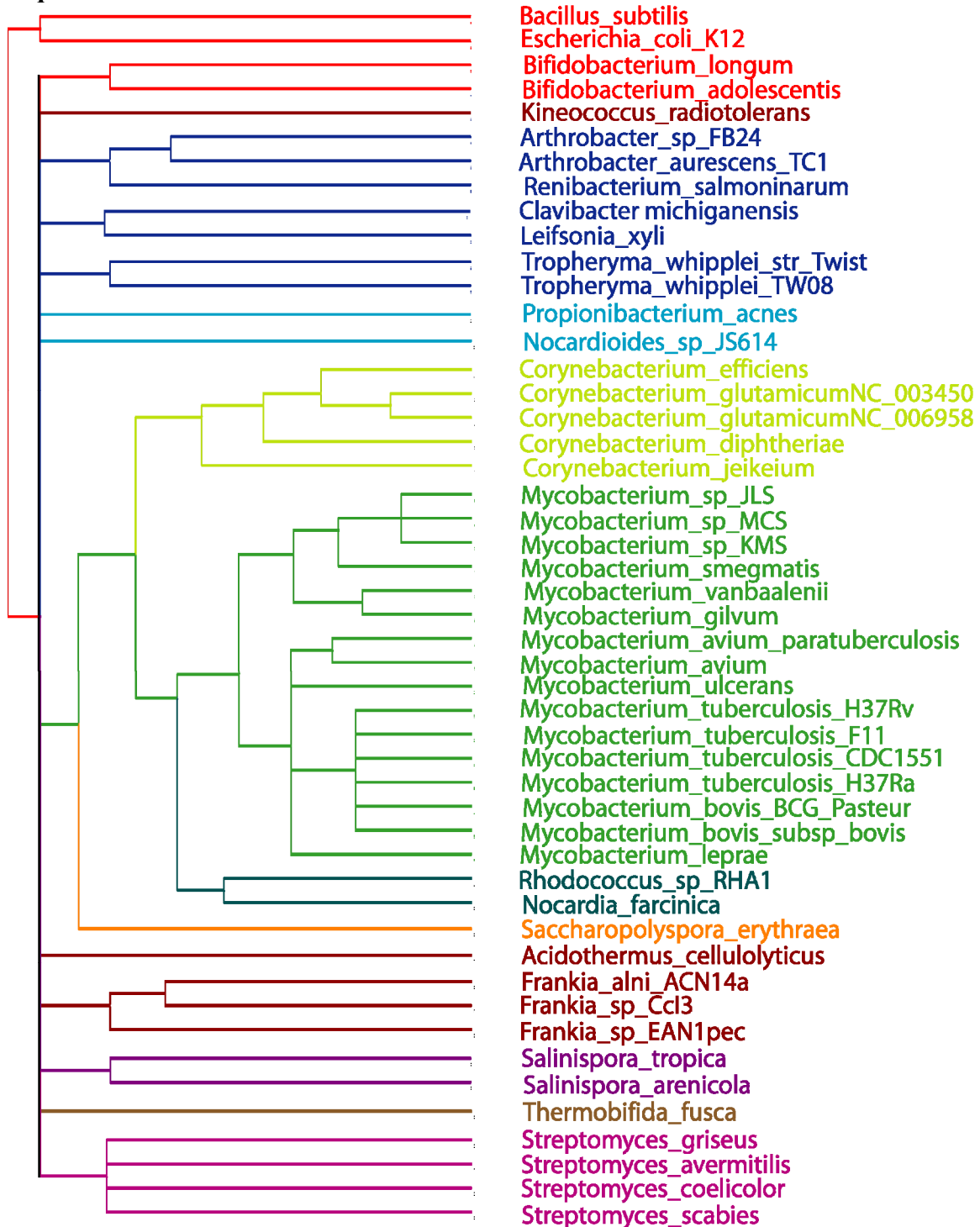
Initial trees were reconstructed using four tree inference approaches (NJ, Fitch, ML, PARS) with 100 bootstrap replicates each and combined by majority-rule consensus to include only well-supported branches. Organisms having the same colors are members of the same suborder in the taxonomical classification of NCBI.

**Supplementary Material Fig 3. Consensus tree based on SecY protein sequence**



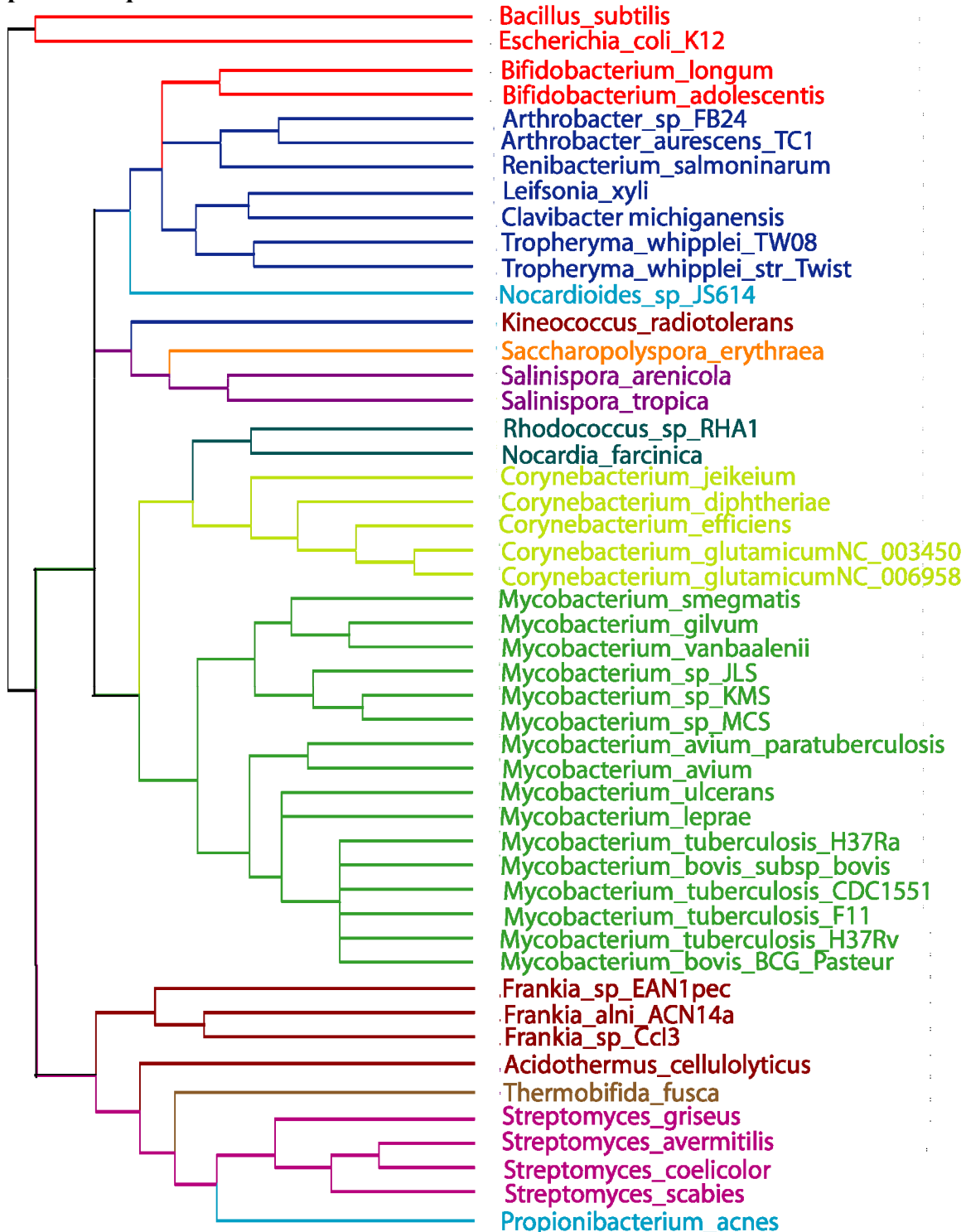
Initial trees were reconstructed using four tree inference approaches (NJ, Fitch, ML, PARS) with 100 bootstrap replicates each and combined by majority-rule consensus to include only well-supported branches. Organisms having the same colors are members of the same suborder in the taxonomical classification of NCBI.

Supplementary Material Fig 4. Consensus tree based on Ribosomal RNA S1 sequence



Initial trees were reconstructed using four tree inference approaches (NJ, Fitch, ML, PARS) with 100 bootstrap replicates each and combined by majority-rule consensus to include only well-supported branches. Organisms having the same colors are members of the same suborder in the taxonomical classification of NCBI.

**Supplementary Material Fig 5. Consensus tree based on Isoleucyl tRNA synthetase protein sequence**



Initial trees were reconstructed using four tree inference approaches (NJ, Fitch, ML, PARS) with 100 bootstrap replicates each and combined by majority-rule consensus to include only well-supported branches. Organisms having the same colors are members of the same suborder in the taxonomical classification of NCBI.